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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/905,744

DATE: 11/21/2001

TIME: 12:14:40

Input Set : N:\Crif3\RULE60\09905744.txt

Output Set: N:\CRF3\11212001\I905744.raw

3 <110> APPLICANT: Chadwick, Brian Paul
 4 Frischauf, Anna-Maria
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
 7 POLYPEPTIDES AND NUCLEIC ACIDS
 9 <130> FILE REFERENCE: 9598-066
 11 <140> CURRENT APPLICATION NUMBER: 09/905,744
 12 <141> CURRENT FILING DATE: 2001-07-13
 14 <150> PRIOR APPLICATION NUMBER: 09/240,639
 15 <151> PRIOR FILING DATE: 1999-01-29
 17 <160> NUMBER OF SEQ ID NOS: 29
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2762
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (232)..(1599)
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 35 ggcgggtgca tggaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttcaga 180
 37 aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaacaag g atg aga 237
 38 Met Arg
 39 1

41 aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc 285
 42 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
 43 5 10 15
 45 ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333
 46 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
 47 20 25 30
 49 cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381
 50 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
 51 35 40 45 50
 53 cgg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429
 54 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
 55 55 60 65
 57 gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc 477
 58 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
 59 70 75 80
 61 act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa 525
 62 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
 63 85 90 95
 65 act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt 573
 66 Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
 67 100 105 110
 69 tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa 621

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70 Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
71 115 120 125 130
73 cta ctg gat gtt gct aaa cag gac att ccc ttc gac ttc tgg aag gcc 669
74 Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
75 135 140 145
77 acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga 717
78 Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
79 150 155 160
81 gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca 765
82 Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
83 165 170 175
85 tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca 813
86 Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
87 180 185 190
89 gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc 861
90 Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
91 195 200 205 210
93 ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga 909
94 Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
95 215 220 225
97 gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag 957
98 Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
99 230 235 240
101 gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc 1005
102 Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
103 245 250 255
105 tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca 1053
106 Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala
107 260 265 270
109 cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga 1101
110 Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
111 275 280 285 290
113 aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg 1149
114 Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
115 295 300 305
117 gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca 1197
118 Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
119 310 315 320
121 agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac 1245
122 Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn
123 325 330 335
125 aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc 1293
126 Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
127 340 345 350
129 tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag 1341
130 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
131 355 360 365 370
133 aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac 1389
134 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr

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135          375          380          385
137 gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc 1437
138 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
139          390          395          400
141 atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc 1485
142 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
143          405          410          415
145 agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc 1533
146 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
147          420          425          430
149 agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga 1581
150 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
151 435          440          445          450
153 cag aag agt cca gcc tca tagtgggcga gccatccctg tccccgtcag 1629
154 Gln Lys Ser Pro Ala Ser
155          455
157 cagtgtctgt gtgtctgcat aaaccctcct gtccctggacg tgacttcac ctaggagacc 1689
159 acagcacagg ccgtctgggc actttctgca cactggctct gggacttgca gaaggcctgg 1749
161 tctgtccctg gcatcagcct cttccagtca catctggcca gagggctgtc tggacctggg 1809
163 cctgtctcaa tgcacctgt ctgcctgggc tccaagtggg caggaccagg acagaaccac 1869
165 aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catccccatg ccccgctccg 1929
167 ggggctgtgg ctgctgtgtg gcatgtccct gcgatgggag tcttgtctcc cagcctgtca 1989
169 gtttccctcc cagggcagag ctccctctcc tgcaagagtc tgggaggcgg tgcaggctgt 2049
171 cctggctgct ctggggaagc cgagggacag ccataacacc cccgggacag taggtctggg 2109
173 cggcaccact gggaaactctg gacttgagtg tgtttgtctt tccctgggta tgaatgtgtg 2169
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185 aggtgcagct gtgccacggg tcagctgagc cacagtccea gaaccaagct ctcggtgtct 2529
187 cgggccacca tccgccacc tggggtgac cccacctcct ccatggacag tgtgagcccc 2589
189 gggccgtgca tctgtctcag tgtggcgta gtgtggggg tgagccccctt gagctgtctt 2649
191 agtgaatgta cagtgtcccg cacgagctga acctcatgtg ttcactccc aataaaaggt 2709
193 tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2762
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197 <211> LENGTH: 456
198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 2
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203 1 5 10 15
205 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
206 20 25 30
208 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
209 35 40 45
211 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
212 50 55 60
214 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala

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215 65 70 75 80
217 Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
218 85 90 95
220 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
221 100 105 110
223 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
224 115 120 125
226 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
227 130 135 140
229 Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
230 145 150 155 160
232 Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
233 165 170 175
235 Lys Ala Ser Pro Phe Leu Val Gly Asp Cys Val Ser Ile Met Asn
236 180 185 190
238 Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
239 195 200 205
241 Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
242 210 215 220
244 Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
245 225 230 235 240
247 Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
248 245 250 255
250 Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
251 260 265 270
253 Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
254 275 280 285
256 Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
257 290 295 300
259 Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
260 305 310 315 320
262 Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
263 325 330 335
265 Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
266 340 345 350
268 Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
269 355 360 365
271 Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
272 370 375 380
274 Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
275 385 390 395 400
277 Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Gln Glu Phe Gly
278 405 410 415
280 Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
281 420 425 430
283 Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
284 435 440 445
286 Asn Arg Gln Lys Ser Pro Ala Ser
287 450 455

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299 <210> SEQ ID NO: 3
291 <211> LENGTH: 2797
292 <212> TYPE: DNA
293 <213> ORGANISM: Homo sapiens
295 <220> FEATURE:
296 <221> NAME/KEY: CDS
297 <222> LOCATION: (83)..(1669)
299 <400> SEQUENCE: 3
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302 ctccgcacag ctaggagaaa ag atg ttc act gtg ctg acc cgc caa cca tgt 112
303 Met Phe Thr Val Leu Thr Arg Gln Pro Cys
304 1 5 10
306 gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc 160
307 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
308 15 20 25
310 ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc 208
311 Leu Val Val Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
312 30 35 40
314 atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt 256
315 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
316 45 50 55
318 att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa 304
319 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
320 60 65 70
322 tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc 352
323 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
324 75 80 85 90
326 aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc 400
327 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
328 95 100 105
330 caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg 448
331 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
332 110 115 120
334 cag qtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc 496
335 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
336 125 130 135
338 acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat 544
339 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
340 140 145 150
342 gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac 592
343 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
344 155 160 165 170
346 ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga 640
347 Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly
348 175 180 185
350 tgg att aca gcc aac tat tta atg gga aat ttc ctg gag aag aac ctg 688
351 Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu
352 190 195 200
354 tgg cac atg tgg gtg cac ccg cat gga gtg gaa acc acg ggt gcc ctg 736

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VERIFICATION SUMMARY

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